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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: NOVARTIS AG
- (B) STREET: SCHWARZWALDALLEE 215
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): 4058
- (G) TELEPHONE: +41 61 324 11 11
- (H) TELEFAX: + 41 61 322 75 32

(ii) TITLE OF INVENTION: Isolation and Characterization of a Gene

(iii) NUMBER OF SEQUENCES: 6

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Oligonucleotide primer DNA (UCPRF)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGGACACCG CCAAAGTCCG

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Oligonucleotide primer DNA (UCPRR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AGCACACAAA CATGATGACG TTCC

24

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: UCP3L

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCCTGGGATG GAGCCCTAGG GAGCCCTGT GCTGCCCTG CCGTGGCAGG ACTCACAGCC	60
CCACCGCTGC ACTGAAGCCC AGGGCTGTGG AGCAGCCTCT CTCCCTGGAC CTCCCTCTCGG	120
CCCTAAAGGG ACTGGGCAGA GCCTTCAGG ACTATGGTTG GACTGAAGCC TTCAAGACGTG	180
CCTCCCCACCA TGGCTGTGAA GTTCCCTGGGG GCAGGCACAG CAGCCTGTT TGCTGACCTC	240
GTTACCTTTC CACTGGACAC AGCCAAGGTC CGCCTGCAGA TCCAGGGGGA GAACCAGGCG	300
GTCCAGACGG CCCGGCTCGT GCAGTACCGT GGC GTGCTGG GCACCATCCT GACCATGGTG	360
CGGACTGAGG GTCCCTGCAG CCCCTACAAT GGGCTGGTGG CGGGCCTGCA GCGCCAGATG	420
AGCTTCCGCT CCATCCGCAT CGGCCTCTAT GACTCCGTCA AGCAGGTGTA CACCCCCAAA	480

GGCGCGGACA ACTCCAGCCT CACTACCCGG ATTTGGCCG GCTGCACCAC AGGAGCCATG	540
GCGGTGACCT GTGCCAGCC CACAGATGTG GTGAAGGTCC GATTCAGGC CAGCATACAC	600
CTCGGGCCAT CCAGGAGCGA CAGAAAATAC AGCGGGACTA TGGACGCCTA CAGAACCATC	660
GCCAGGGAGG AAGGAGTCAG GGGCCTGTGG AAAGGAACCT TGCCCAACAT CATGAGGAAT	720
GCTATCGTCA ACTGTGCTGA GGTGGTGACC TACCGACATCC TCAAGGAGAA GCTGCTGGAC	780
TACCACCTGC TCACTGACAA CTTCCCCCTGC CACTTTGTCT CTGCCTTGG AGCCGGCTTC	840
TGTGCCACAG TGGTGGCCTC CCCGGTGGAC GTGGTGAAGA CCCGGTATAT GAACTCACCT	900
CCAGGCCAGT ACTTCAGCCC CCTCGACTGT ATGATAAAGA TGGTGGCCCA GGAGGGCCCC	960
ACAGCCTTCT ACAAGGGATT TACACCCCTCC TTTTTGCGTT TGGGATCCTG GAACGTGGTG	1020
ATGTTCGTAA CCTATGAGCA GCTGAAACGG GCCCTGATGA AAGTCCAGAT GTTACGGGAA	1080
TCACCGTTT GAACAAGACA AGAAGGCCAC TGGTAGCTAA CGTGTCCGAA ACCAGTTAAG	1140
AATGGAAGAA AACGGTGCAT CCACGCACAC ATGGACACAG ACCCACACAT GTTTACAGAA	1200
CTGTTGTTTA CTTGTTGCTG ATTCAAGAAA C	1231

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: UCP3L

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Val Gly Leu Lys Pro Ser Asp Val Pro Pro Thr Met Ala Val Lys			
1	5	10	15

Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala Asp Leu Val Thr Phe

20	25	30
Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln		
35	40	45
Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr		
50	55	60
Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly		
65	70	75
Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile		
85	90	95
Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp		
100	105	110
Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala		
115	120	125
Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe		
130	135	140
Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser		
145	150	155
160		
Gly Thr Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg		
165	170	175
Gly Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val		
180	185	190
Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu		
195	200	205
Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala		
210	215	220
Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val		
225	230	235
240		
Val Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro		
245	250	255
Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe		
260	265	270
Tyr Lys Gly Phe Thr Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val		
275	280	285
Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Lys Val		
290	295	300
Gln Met Leu Arg Glu Ser Pro Phe		
305	310	

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: UCP3S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TCCTGGGATG GAGCCCTAGG GAGCCCCTGT GCTGCCCTG CCGTGGCAGG ACTCACAGCC	60
CCACCGCTGC ACTGAAGCCC AGGGCTGTGG AGCAGCCTCT CTCCCTGGAC CTCCCTCTCGG	120
CCCTAAAGGG ACTGGGCAGA GCCTTCCAGG ACTATGGTTG GACTGAAGCC TTCAAGACGTG	180
CCTCCCCACCA TGGCTGTGAA GTTCCTGGGG GCAGGCACAG CAGCCTGTTT TGCTGACCTC	240
GTTACCTTTC CACTGGACAC AGCCAAGGTC CGCCTGCAGA TCCAGGGGA GAACCAGGCG	300
GTCCAGACGG CCCGGCTCGT GCAGTACCGT GGCCTGCTGG GCACCATCCT GACCATGGTG	360
CGGACTGAGG GTCCCTGCAG CCCCTACAAT GGGCTGGTGG CCGGCCTGCA GCGCCAGATG	420
AGCTTCGCCT CCATCCGCAT CGGCCTCTAT GACTCCGTCA AGCAGGTGTA CACCCCCAAA	480
GGCGCGGACA ACTCCAGCCT CACTACCCGG ATTTTGGCCG GCTGCACCAAC AGGAGCCATG	540
GCGGTGACCT GTGCCCTAGCC CACAGATGTG GTGAAGGTCC GATTTCAGGC CAGCATAACAC	600
CTCGGGCCAT CCAGGAGCGA CAGAAAATAC AGCGGGACTA TGGACGCCTA CAGAACCATC	660
GCCAGGGAGG AAGGAGTCAG GGGCCTGTGG AAAGGAACCT TGCCCAACAT CATGAGGAAT	720
GCTATCGTCA ACTGTGCTGA GGTGGTGACC TACGACATCC TCAAGGAGAA GCTGCTGGAC	780
TACCACCTGC TCACTGACAA CTTCCCTGTC CACTTTGTCT CTGCCTTGG AGCCGGCTTC	840
TGTGCCACAG TGGTGGCCTC CCCGGTGGAC GTGGTGAAGA CCCGGTATAT GAACTCACCT	900
CCAGGCCAGT ACTTCAGCCC CCTCGACTGT ATGATAAAGA TGGTGGCCCA GGAGGGCCCC	960

ACAGCCCTCT ACAAGGGGTG AGCCTCCCTCC TGCCTCCAGC ACTCCCTCCC AGAGAACAGG	1020
GGCTTCTTTC TTTCGAATG TGGCTACCGT GGGTCAACCT GGGATGTAGC GGTGAAGAGT	1080
ACAGATGTAA ATGCCACAAA GAAGAAGTTT AAAAAACCAT GCAAAAAAAA AA	1132

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: UCP3S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Val Gly Leu Lys Pro Ser Asp Val Pro Pro Thr Met Ala Val Lys			
1	5	10	15

Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala Asp Leu Val Thr Phe		
20	25	30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln		
35	40	45

Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr		
50	55	60

Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly			
65	70	75	80

Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile		
85	90	95

Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp		
100	105	110

Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala		
115	120	125

Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe	
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130	135	140	
Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser			
145	150	155	160
Gly Thr Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg			
165	170	175	
Gly Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val			
180	185	190	
Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu			
195	200	205	
Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala			
210	215	220	
Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val			
225	230	235	240
Val Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro			
245	250	255	
Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe			
260	265	270	
Tyr Lys Gly			
275			